

Sequence Listing

<110> Botstein,David
Desnoyers,Luc
Ferrara,Napoleone
Fong,Sherman
Gao,Wei-Qiang
Goddard,Audrey
Gurney,Austin L.
Pan,James
Roy,Margaret Ann
Stewart,Timothy A.
Tumas,Daniel
Watanabe,Colin K.
Wood,William I.

<120> Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same

<130> P2930R1C6

<150> 60/095,325

<151> 1998-08-04

<150> 60/112,851

<151> 1998-12-16

<150> 60/113,145

<151> 1998-12-16

<150> 60/113,511

<151> 1998-12-22

<150> 60/115,558

<151> 1999-01-12

<150> 60/115,565

<151> 1999-01-12

<150> 60/115,733

<151> 1999-01-12

<150> 60/119,341

<151> 1999-02-09

11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

<151> 2000-03-03

<150> PCT/US99/12252

<151> 1999-06-02

<150> PCT/US99/28634

<151> 1999-12-01

<150> PCT/US99/28551

<151> 1999-12-02

<150> PCT/US00/03565

<151> 2000-02-11

<150> PCT/US00/04414

<151> 2000-02-22

<150> PCT/US00/05841

<151> 2000 -03-02

<150> PCT/US00/08439

<151> 2000-03-30

<150> PCT/US00/14941

<151> 2000-05-30

<150> PCT/US00/15264

<151> 2000-06-02

<150> PCT/US00/32678

<151> 2000-12-01

<140> US 09/866,034

<141> 2001-05-25

<160> 38

<210> 1

<211> 1283

<212> DNA

<213> Homo sapiens

<400> 1

cggacgcgtg ggacccatac ttgctggtct gatccatgca caaggcgggg 50

ctgctaggcc tctgtgcccg ggcttggaat tcggtgcgga tggccagctc 100

cgggatgacc cgccgggacc cgctcgcaaa taagggtggcc ctggtaacgg 150

cctccaccga cgggatcggc ttgccatcg cccggcggtt ggcccaggac 200

ggggcccatg tggctgctcag cagccggaag cagcagaatg tggaccaggc 250

ggtggccacg ctgcaggggg aggggctgag cgtgacgggc accgtgtgcc 300

atgtggggaa ggcggaggac cgggagcggc tgggtggccac ggctgtgaag 350

```

cttcatggag gtatcgatat cctagtctcc aatgetgctg tcaacccttt 400
ctttggaagc ataatggatg tcaactgagga ggtgtgggac aagactctgg 450
acattaatgt gaaggcccca gccctgatga caaaggcagt ggtgccagaa 500
atggagaaac gaggaggcgg ctcaagtgtg atcgtgtctt ccatagcagc 550
cttcagtcca tctcctgggt tcagtcctta caatgtcagt aaaacagcct 600
tgctggggcct gaccaagacc ctggccatag agctggcccc aaggaacatt 650
aggggtgaact gcctagcacc tggacttatc aagactagct tcagcaggat 700
gctctggatg gacaaggaaa aagaggaaa catgaaagaa accctgcgga 750
taagaagggt aggcgagcca gaggattgtg ctggcatcgt gtctttcctg 800
tgctctgaag atgccagcta catcactggg gaaacagtgg tgggtgggtg 850
aggaaccccg tcccgctctt gaggaccggg agacagccca caggccagag 900
ttgggctcta gctcctgggt ctgttctctg attcaccac tggcctttcc 950
cacctctgct caccttactg ttcacctcat caaatcagtt ctgcctgtg 1000
aaaagatcca gccttccttg cgtcaagggt ggcgtcttac tcgggattcc 1050
tgctgttggt gtggccttgg gtaaaggcct ccctgagaa cacaggacag 1100
gcctgctgac aaggctgagt ctaccttggc aaagaccaag atattttttc 1150
ctgggccact ggtgaatctg aggggtgatg ggagagaagg aacctggagt 1200
ggaaggagca gagttgcaaa ttaacagctt gcaaagagg tgcaaataaa 1250
atgcagatga ttgcgcggct ttgaaaaaaa aaa 1283

```

<210> 2

<211> 278

<212> PRT

<213> Homo sapiens

<400> 2

```

Met His Lys Ala Gly Leu Leu Gly Leu Cys Ala Arg Ala Trp Asn
  1             5             10             15
Ser Val Arg Met Ala Ser Ser Gly Met Thr Arg Arg Asp Pro Leu
          20             25             30
Ala Asn Lys Val Ala Leu Val Thr Ala Ser Thr Asp Gly Ile Gly
          35             40             45
Phe Ala Ile Ala Arg Arg Leu Ala Gln Asp Gly Ala His Val Val
          50             55             60
Val Ser Ser Arg Lys Gln Gln Asn Val Asp Gln Ala Val Ala Thr
          65             70             75

```

Leu	Gln	Gly	Glu	Gly	Leu	Ser	Val	Thr	Gly	Thr	Val	Cys	His	Val	80	85	90
Gly	Lys	Ala	Glu	Asp	Arg	Glu	Arg	Leu	Val	Ala	Thr	Ala	Val	Lys	95	100	105
Leu	His	Gly	Gly	Ile	Asp	Ile	Leu	Val	Ser	Asn	Ala	Ala	Val	Asn	110	115	120
Pro	Phe	Phe	Gly	Ser	Ile	Met	Asp	Val	Thr	Glu	Glu	Val	Trp	Asp	125	130	135
Lys	Thr	Leu	Asp	Ile	Asn	Val	Lys	Ala	Pro	Ala	Leu	Met	Thr	Lys	140	145	150
Ala	Val	Val	Pro	Glu	Met	Glu	Lys	Arg	Gly	Gly	Gly	Ser	Val	Val	155	160	165
Ile	Val	Ser	Ser	Ile	Ala	Ala	Phe	Ser	Pro	Ser	Pro	Gly	Phe	Ser	170	175	180
Pro	Tyr	Asn	Val	Ser	Lys	Thr	Ala	Leu	Leu	Gly	Leu	Thr	Lys	Thr	185	190	195
Leu	Ala	Ile	Glu	Leu	Ala	Pro	Arg	Asn	Ile	Arg	Val	Asn	Cys	Leu	200	205	210
Ala	Pro	Gly	Leu	Ile	Lys	Thr	Ser	Phe	Ser	Arg	Met	Leu	Trp	Met	215	220	225
Asp	Lys	Glu	Lys	Glu	Glu	Ser	Met	Lys	Glu	Thr	Leu	Arg	Ile	Arg	230	235	240
Arg	Leu	Gly	Glu	Pro	Glu	Asp	Cys	Ala	Gly	Ile	Val	Ser	Phe	Leu	245	250	255
Cys	Ser	Glu	Asp	Ala	Ser	Tyr	Ile	Thr	Gly	Glu	Thr	Val	Val	Val	260	265	270
Gly	Gly	Gly	Thr	Pro	Ser	Arg	Leu								275		

<210> 3
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 3
 gcataatgga tgtcactgag g 21

 <210> 4
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 4
agaacaatcc tgctgaaagc tag 23

<210> 5
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 5
gaaacgagga ggcggctcag tggatgatcgt gtcttccata gcagcc 46

<210> 6
<211> 3121
<212> DNA
<213> Homo sapiens

<400> 6
gcgccttgag ctccgcctcc gggcccgata gcggcatcga gagegcctcc 50
gtcgaggacc aggcggcgca gggggccggc gggcgaaagg aggatgaggg 100
ggcgagcag ctgctgacct tgcagaacca ggtggcgagg ctggaggagg 150
agaaccgaga ctttctggct gcgctggagg acgccatgga gcagtacaaa 200
ctgcagagcg accggctgag tgagcagcag gaggagatgg tggaactgag 250
gctgcggtta gagctggtgc ggccaggctg ggggggctg cggctcctga 300
atggcctgcc tcccggtcc tttgtgctc gacctcctac agccccctg 350
gggggtgccc acgcccattg gctgggcatg gtgcgcctg cctgcctccc 400
tgagatgaa gttggctctg agcagagggg agagcaggtg acaaattggc 450
gggaggctgg agctgagttg ctgactgagg tgaacaggct gggaagtggc 500
tcttcagctg cttcagagga ggaagaggag gaggaggagc cggccaggcg 550
gaccttacac ctgcgcagaa ataggatcag caactgcagt cagagggcgg 600
gggcacgccc agggagtctg ccagagagga agggcccaga gctttgcctt 650
gaggagtgg atgcagccat tccagggtcc agagcagttg gtgggagcaa 700
ggcccagatt caggcccgcc aggtcccccc tgccacagcc tcagagtggc 750
ggctggcca gggcagcag aagatccggg agctggctat caacatccgc 800
atgaaggagg agcttattgg cgagctggc cgcacaggaa aggcagctca 850
ggcctgaac cgccagcaca gccagcgtat ccgggagctg gagcaggagg 900

tcctggaaat gaagatgagc tccacctggc acccgagctt ctctggctgt 2400
 cccccctcac tgaggggggcc ccccgacccc gggaggagac gcgggacttg 2450
 gtccacgctc cgttaccctt gacctggaaa cgctcgagcc tgtgtggtga 2500
 ggagcagggg tcccccgagg aactgaggca gcgggaggcg gctgagcccc 2550
 tggtagggcg ggtgcttctt gtgggtgagg caggcctgcc ctggaacttt 2600
 gggcctttgt ccaagccccg gcggaactg cgacgagcca gcccgggat 2650
 gattgatgtc cggaataacc cctgtaagc cctcggggca gacctgcct 2700
 tggagggaga ctccgagcct gctgaaaggg gcagctgcct gttttgcttc 2750
 tgtgaagggc agtccttacc gcacacctta aatccaggcc ctcatctgta 2800
 cctcactgg gatcaacaaa tttgggcat ggccaaaag aactggaccc 2850
 tcatttaaca aaataatatg caaattccca ccacttactt ccatgaagct 2900
 gtggtaccca attgccgctt tgtgtcttgc tcgaatctca ggacaattct 2950
 ggtttcaggc gtaaattggat gtgctttag ttcaggggtt tggccaagaa 3000
 tcatcacgaa agggctcggg gcaaccaggt tgtggtttaa atgggtcttat 3050
 gtatataggg gaaactggga gacttttaga tcttaaaaaa ccatttaata 3100
 aaaaaaatc tttgaaggga c 3121

<210> 7

<211> 830

<212> PRT

<213> Homo sapiens

<400> 7

Met	Glu	Gln	Tyr	Lys	Leu	Gln	Ser	Asp	Arg	Leu	Arg	Glu	Gln	Gln
1				5					10				15	
Glu	Glu	Met	Val	Glu	Leu	Arg	Leu	Arg	Leu	Glu	Leu	Val	Arg	Pro
			20					25					30	
Gly	Trp	Gly	Gly	Leu	Arg	Leu	Leu	Asn	Gly	Leu	Pro	Pro	Gly	Ser
			35					40					45	
Phe	Val	Pro	Arg	Pro	His	Thr	Ala	Pro	Leu	Gly	Gly	Ala	His	Ala
			50					55					60	
His	Val	Leu	Gly	Met	Val	Pro	Pro	Ala	Cys	Leu	Pro	Gly	Asp	Glu
			65					70					75	
Val	Gly	Ser	Glu	Gln	Arg	Gly	Glu	Gln	Val	Thr	Asn	Gly	Arg	Glu
			80					85					90	
Ala	Gly	Ala	Glu	Leu	Leu	Thr	Glu	Val	Asn	Arg	Leu	Gly	Ser	Gly
			95					100					105	

Ser Ser Ala Ala	Ser Glu Glu Glu Glu Glu Glu Glu Glu	Pro Pro
110	115	120
Arg Arg Thr Leu His	Leu Arg Arg Asn Arg Ile Ser Asn Cys Ser	
125	130	135
Gln Arg Ala Gly Ala Arg	Pro Gly Ser Leu Pro Glu Arg Lys Gly	
140	145	150
Pro Glu Leu Cys Leu Glu Glu Leu Asp	Ala Ala Ile Pro Gly Ser	
155	160	165
Arg Ala Val Gly Gly Ser Lys Ala Arg	Val Gln Ala Arg Gln Val	
170	175	180
Pro Pro Ala Thr Ala Ser Glu Trp Arg	Leu Ala Gln Ala Gln Gln	
185	190	195
Lys Ile Arg Glu Leu Ala Ile Asn Ile	Arg Met Lys Glu Glu Leu	
200	205	210
Ile Gly Glu Leu Val Arg Thr Gly Lys	Ala Ala Gln Ala Leu Asn	
215	220	225
Arg Gln His Ser Gln Arg Ile Arg Glu	Leu Glu Gln Glu Ala Glu	
230	235	240
Gln Val Arg Ala Glu Leu Ser Glu Gly	Gln Arg Gln Leu Arg Glu	
245	250	255
Leu Glu Gly Lys Glu Leu Gln Asp Ala	Gly Glu Arg Ser Arg Leu	
260	265	270
Gln Glu Phe Arg Arg Arg Val Ala Ala	Ala Gln Ser Gln Val Gln	
275	280	285
Val Leu Lys Glu Lys Lys Gln Ala Thr	Glu Arg Leu Val Ser Leu	
290	295	300
Ser Ala Gln Ser Glu Lys Arg Leu Gln	Glu Leu Glu Arg Asn Val	
305	310	315
Gln Leu Met Arg Gln Gln Gln Gly Gln	Leu Gln Arg Arg Leu Arg	
320	325	330
Glu Glu Thr Glu Gln Lys Arg Arg Leu	Glu Ala Glu Met Ser Lys	
335	340	345
Arg Gln His Arg Val Lys Glu Leu Glu	Leu Lys His Glu Gln Gln	
350	355	360
Gln Lys Ile Leu Lys Ile Lys Thr Glu	Glu Ile Ala Ala Phe Gln	
365	370	375
Arg Lys Arg Arg Ser Gly Ser Asn Gly	Ser Val Val Ser Leu Glu	
380	385	390
Gln Gln Gln Lys Ile Glu Glu Gln Lys Lys	Trp Leu Asp Gln Glu	

395	400	405
Met Glu Lys Val Leu Gln Gln Arg Arg	Ala Leu Glu Glu Leu Gly	
410	415	420
Glu Glu Leu His Lys Arg Glu Ala Ile	Leu Ala Lys Lys Glu Ala	
425	430	435
Leu Met Gln Glu Lys Thr Gly Leu Glu	Ser Lys Arg Leu Arg Ser	
440	445	450
Ser Gln Ala Leu Asn Glu Asp Ile Val	Arg Val Ser Ser Arg Leu	
455	460	465
Glu His Leu Glu Lys Glu Leu Ser Glu	Lys Ser Gly Gln Leu Arg	
470	475	480
Gln Gly Ser Ala Gln Ser Gln Gln Gln	Ile Arg Gly Glu Ile Asp	
485	490	495
Ser Leu Arg Gln Glu Lys Asp Ser Leu	Leu Lys Gln Arg Leu Glu	
500	505	510
Ile Asp Gly Lys Leu Arg Gln Gly Ser	Leu Leu Ser Pro Glu Glu	
515	520	525
Glu Arg Thr Leu Phe Gln Leu Asp Glu	Ala Ile Glu Ala Leu Asp	
530	535	540
Ala Ala Ile Glu Tyr Lys Asn Glu Ala	Ile Thr Cys Arg Gln Arg	
545	550	555
Val Leu Arg Ala Ser Ala Ser Leu Leu	Ser Gln Cys Glu Met Asn	
560	565	570
Leu Met Ala Lys Leu Ser Tyr Leu Ser	Ser Ser Glu Thr Arg Ala	
575	580	585
Leu Leu Cys Lys Tyr Phe Asp Lys Val	Val Thr Leu Arg Glu Glu	
590	595	600
Gln His Gln Gln Gln Ile Ala Phe Ser	Glu Leu Glu Met Gln Leu	
605	610	615
Glu Glu Gln Gln Arg Leu Val Tyr Trp	Leu Glu Val Ala Leu Glu	
620	625	630
Arg Gln Arg Leu Glu Met Asp Arg Gln	Leu Thr Leu Gln Gln Lys	
635	640	645
Glu His Glu Gln Asn Met Gln Leu Leu	Leu Gln Gln Ser Arg Asp	
650	655	660
His Leu Gly Glu Gly Leu Ala Asp Ser	Arg Arg Gln Tyr Glu Ala	
665	670	675
Arg Ile Gln Ala Leu Glu Lys Glu Leu	Gly Arg Tyr Met Trp Ile	
680	685	690

Asn	Gln	Glu	Leu	Lys	Gln	Lys	Leu	Gly	Gly	Val	Asn	Ala	Val	Gly	
				695					700					705	
His	Ser	Arg	Gly	Gly	Glu	Lys	Arg	Ser	Leu	Cys	Ser	Glu	Gly	Arg	
				710					715					720	
Gln	Ala	Pro	Gly	Asn	Glu	Asp	Glu	Leu	His	Leu	Ala	Pro	Glu	Leu	
				725					730					735	
Leu	Trp	Leu	Ser	Pro	Leu	Thr	Glu	Gly	Ala	Pro	Arg	Thr	Arg	Glu	
				740					745					750	
Glu	Thr	Arg	Asp	Leu	Val	His	Ala	Pro	Leu	Pro	Leu	Thr	Trp	Lys	
				755					760					765	
Arg	Ser	Ser	Leu	Cys	Gly	Glu	Glu	Gln	Gly	Ser	Pro	Glu	Glu	Leu	
				770					775					780	
Arg	Gln	Arg	Glu	Ala	Ala	Glu	Pro	Leu	Val	Gly	Arg	Val	Leu	Pro	
				785					790					795	
Val	Gly	Glu	Ala	Gly	Leu	Pro	Trp	Asn	Phe	Gly	Pro	Leu	Ser	Lys	
				800					805					810	
Pro	Arg	Arg	Glu	Leu	Arg	Arg	Ala	Ser	Pro	Gly	Met	Ile	Asp	Val	
				815					820					825	
Arg	Lys	Asn	Pro	Leu											
				830											

<210> 8
 <211> 662
 <212> DNA
 <213> Homo sapiens

<400> 8
 attctcctag agcatctttg gaagcatgag gccacgatgc tgcattcttg 50
 ctcttgctctg ctggataaca gtcttctctcc tccagtgttc aaaaggaact 100
 acagacgctc ctgttggctc aggactgtgg ctgtgccagc cgacaccag 150
 gtgtgggaac aagatctaca acccttcaga gcagtgtctg tatgatgatg 200
 ccatcttata cttaaaggag accgcgcgt gtggctccac ctgcaccttc 250
 tggcctgct ttgagctctg ctgtcccag tcttttggcc cccagcagaa 300
 gtttcttggtg aagttgaggg ttctgggtat gaagtctcag tgtcacttat 350
 ctcccatctc cggagctgt accaggaaca ggaggcacgt cctgtacca 400
 taaaaacccc aggtccact ggcagacggc agacaagggg agaagagacg 450
 aagcagctgg acatcggaga ctacagttga acttcggaga gaagcaactt 500
 gacttcagag ggatggctca atgacatagc tttggagagg agcccagctg 550

gggatggcca gacttcaggg gaagaatgcc ttctgcttc atcccccttc 600
 cagctccccct tcccgctgag agccactttc atcggaata aaatccccca 650
 catttaccat ct 662

<210> 9
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 9
 Met Arg Pro Arg Cys Cys Ile Leu Ala Leu Val Cys Trp Ile Thr
 1 5 10 15
 Val Phe Leu Leu Gln Cys Ser Lys Gly Thr Thr Asp Ala Pro Val
 20 25 30
 Gly Ser Gly Leu Trp Leu Cys Gln Pro Thr Pro Arg Cys Gly Asn
 35 40 45
 Lys Ile Tyr Asn Pro Ser Glu Gln Cys Cys Tyr Asp Asp Ala Ile
 50 55 60
 Leu Ser Leu Lys Glu Thr Arg Arg Cys Gly Ser Thr Cys Thr Phe
 65 70 75
 Trp Pro Cys Phe Glu Leu Cys Cys Pro Glu Ser Phe Gly Pro Gln
 80 85 90
 Gln Lys Phe Leu Val Lys Leu Arg Val Leu Gly Met Lys Ser Gln
 95 100 105
 Cys His Leu Ser Pro Ile Ser Arg Ser Cys Thr Arg Asn Arg Arg
 110 115 120
 His Val Leu Tyr Pro
 125

<210> 10
 <211> 1942
 <212> DNA
 <213> Homo sapiens

<400> 10
 cccacgcgtc cgcccacgag tccgggtgcc actcgcgcg cgcccgcgct 50
 ccgggcttct cttttccctc cgacgcgcca cggtgcca gacattccgg 100
 ctgccgggtc tggagagctc cccgaacccc tccgcggaga ggagcgaggc 150
 ggcgccaggg tggcccccg ggcgcgcttg gtctcgga agcggggacg 200
 aggcgggagg atgagcgact gagggcgacg cgggcactga cgcgagttgg 250
 ggccgcgact accggcagct gacagcgca tgagcgactc cccagagacg 300
 ccctagcccc gtgtgcgcgc caggcggagc gcgcaggtgg ggctgggctg 350

agtacacaaa agtacactat tatatatcaa atgtatttct ataatccctc 1850
cattagagag cttatataag tgttttctat agatgcagat taaaaatgct 1900
gtgttgtcaa ccgtcaaaaa aaaaaaaaaa aaaaaaaaaa aa 1942

<210> 11
<211> 325
<212> PRT
<213> Homo sapiens

<400> 11

Met	Pro	Ser	Ser	Thr	Ala	Met	Ala	Val	Gly	Ala	Leu	Ser	Ser	Ser	1	5	10	15
Leu	Leu	Val	Thr	Cys	Cys	Leu	Met	Val	Ala	Leu	Cys	Ser	Pro	Ser	20	25	30	
Ile	Pro	Leu	Glu	Lys	Leu	Ala	Gln	Ala	Pro	Glu	Gln	Pro	Gly	Gln	35	40	45	
Glu	Lys	Arg	Glu	His	Ala	Thr	Arg	Asp	Gly	Pro	Gly	Arg	Val	Asn	50	55	60	
Glu	Leu	Gly	Arg	Pro	Ala	Arg	Asp	Glu	Gly	Gly	Ser	Gly	Arg	Asp	65	70	75	
Trp	Lys	Ser	Lys	Ser	Gly	Arg	Gly	Leu	Ala	Gly	Arg	Glu	Pro	Trp	80	85	90	
Ser	Lys	Leu	Lys	Gln	Ala	Trp	Val	Ser	Gln	Gly	Gly	Gly	Ala	Lys	95	100	105	
Ala	Gly	Asp	Leu	Gln	Val	Arg	Pro	Arg	Gly	Asp	Thr	Pro	Gln	Ala	110	115	120	
Glu	Ala	Leu	Ala	Ala	Ala	Gln	Asp	Ala	Ile	Gly	Pro	Glu	Leu	125	130	135		
Ala	Pro	Thr	Pro	Glu	Pro	Pro	Glu	Glu	Tyr	Val	Tyr	Pro	Asp	Tyr	140	145	150	
Arg	Gly	Lys	Gly	Cys	Val	Asp	Glu	Ser	Gly	Phe	Val	Tyr	Ala	Ile	155	160	165	
Gly	Glu	Lys	Phe	Ala	Pro	Gly	Pro	Ser	Ala	Cys	Pro	Cys	Leu	Cys	170	175	180	
Thr	Glu	Glu	Gly	Pro	Leu	Cys	Ala	Gln	Pro	Glu	Cys	Pro	Arg	Leu	185	190	195	
His	Pro	Arg	Cys	Ile	His	Val	Asp	Thr	Ser	Gln	Cys	Cys	Pro	Gln	200	205	210	
Cys	Lys	Glu	Arg	Lys	Asn	Tyr	Cys	Glu	Phe	Arg	Gly	Lys	Thr	Tyr	215	220	225	
Gln	Thr	Leu	Glu	Glu	Phe	Val	Val	Ser	Pro	Cys	Glu	Arg	Cys	Arg				

230	235	240
Cys Glu Ala Asn Gly Glu Val Leu Cys	Thr Val Ser Ala Cys	Pro
245	250	255
Gln Thr Glu Cys Val Asp Pro Val Tyr	Glu Pro Asp Gln Cys	Cys
260	265	270
Pro Ile Cys Lys Asn Gly Pro Asn Cys	Phe Ala Glu Thr Ala	Val
275	280	285
Ile Pro Ala Gly Arg Glu Val Lys Thr	Asp Glu Cys Thr Ile	Cys
290	295	300
His Cys Thr Tyr Glu Glu Gly Thr Trp	Arg Ile Glu Arg Gln	Ala
305	310	315
Met Cys Thr Arg His Glu Cys Arg Gln	Met	
320	325	

<210> 12
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 12
 gaggtgtcgc tgtgaagcca acgg 24

<210> 13
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 13
 cgctcgattc tccatgtgcc ttcc 24

<210> 14
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 14
 gacggagtgt gtggaccctg tgtacgagcc tgatcagtgc tgtcc 45

<210> 15
 <211> 1587
 <212> DNA
 <213> Homo sapiens

<400> 15

cagccacaga cgggtcatga gcgcggtatt actgctggcc ctcttggggt 50
tcctctccc actgccagga gtgcaggcgc tgctctgcca gtttgggaca 100
gttcagcatg tgtggaaggt gtccgacctc ccccggaat ggacccctaa 150
gaacaccagc tgcgacagcg gcttgggggtg ccaggacacg ttgatgctca 200
ttgagagcgg accccaagtg agcctgggtgc tctccaaggg ctgcacggag 250
gccaaggacc aggagccccg cgtcactgag caccggatgg gccccggcct 300
ctcctgata tctacacct tegtgtgccg ccaggaggac ttctgcaaca 350
acctcgtaa ctccctcccg ctttggggcc cacagcccc agcagacca 400
ggatccttga ggtgccagt ctgcttgtct atggaaggct gtctggaggg 450
gacaacagaa gagatctgcc ccaaggggac cacacactgt tatgatggcc 500
tcctcaggct caggggagga ggcattctct ccaatctgag agtccaggga 550
tgcatgcccc agccagggtg caacctgctc aatgggacac aggaaattgg 600
gcccgtgggt atgactgaga actgcaatag gaaagatttt ctgacctgtc 650
atcgggggac caccattatg acacacggaa acttggctca agaaccact 700
gattggacca catcgaatac cgagatgtgc gaggtggggc aggtgtgtca 750
ggagacgtg ctgctcatag atgtaggact cacatcaacc ctgggtgggga 800
caaaaggctg cagcactgtt ggggctcaaa attcccagaa gaccaccatc 850
cactcagccc ctcttggggt gcttgtggcc tctataccc acttctgctc 900
ctcggacctg tgcaatagt ccagcagcag cagcgttctg ctgaactccc 950
tcctctctca agctgcccct gtcccaggag accggcagtg tctacctgt 1000
gtgcagcccc ttggaacctg ttcaagtggc tcccccgaa tgacctgcc 1050
caggggcgcc actcattgtt atgatgggtc cattcatctc tcaggaggtg 1100
ggctgtccac caaatgagc attcagggtg gcgtggccca acctccagc 1150
ttcttgttga accacaccag acaaatcggg atcttctctg cgcgtgagaa 1200
gcgtgatgtg cagcctctg cctctcagca tgaggaggt ggggctgagg 1250
gcctggagtc tctcacttgg ggggtggggc tggcactggc ccagcgtg 1300
tggtggggag tggtttgcct tctctgctaa ctctattacc ccacgattc 1350
ttcaccgctg ctgaccacc aactcaacc tccctctgac ctcataacct 1400
aatggccttg gacaccagat tctttccat tctgtccatg aatcatcttc 1450

cccacacaca atcattcata tctactcacc taacagcaac actggggaga 1500
gcttgaggca tccggacttg ccctatggga gaggggacgc tggaggagtg 1550
gctgcattga tctgataata cagaccctgt cctttca 1587

<210> 16
<211> 437
<212> PRT
<213> Homo sapiens

<400> 16
Met Ser Ala Val Leu Leu Leu Ala Leu Leu Gly Phe Ile Leu Pro
1 5 10 15
Leu Pro Gly Val Gln Ala Leu Leu Cys Gln Phe Gly Thr Val Gln
20 25 30
His Val Trp Lys Val Ser Asp Leu Pro Arg Gln Trp Thr Pro Lys
35 40 45
Asn Thr Ser Cys Asp Ser Gly Leu Gly Cys Gln Asp Thr Leu Met
50 55 60
Leu Ile Glu Ser Gly Pro Gln Val Ser Leu Val Leu Ser Lys Gly
65 70 75
Cys Thr Glu Ala Lys Asp Gln Glu Pro Arg Val Thr Glu His Arg
80 85 90
Met Gly Pro Gly Leu Ser Leu Ile Ser Tyr Thr Phe Val Cys Arg
95 100 105
Gln Glu Asp Phe Cys Asn Asn Leu Val Asn Ser Leu Pro Leu Trp
110 115 120
Ala Pro Gln Pro Pro Ala Asp Pro Gly Ser Leu Arg Cys Pro Val
125 130 135
Cys Leu Ser Met Glu Gly Cys Leu Glu Gly Thr Thr Glu Glu Ile
140 145 150
Cys Pro Lys Gly Thr Thr His Cys Tyr Asp Gly Leu Leu Arg Leu
155 160 165
Arg Gly Gly Gly Ile Phe Ser Asn Leu Arg Val Gln Gly Cys Met
170 175 180
Pro Gln Pro Gly Cys Asn Leu Leu Asn Gly Thr Gln Glu Ile Gly
185 190 195
Pro Val Gly Met Thr Glu Asn Cys Asn Arg Lys Asp Phe Leu Thr
200 205 210
Cys His Arg Gly Thr Thr Ile Met Thr His Gly Asn Leu Ala Gln
215 220 225
Glu Pro Thr Asp Trp Thr Thr Ser Asn Thr Glu Met Cys Glu Val

-11- gctg gctg gctg gctg gctg gctg -11-
 -12- gctg gctg gctg gctg gctg gctg -12-
 -13- gctg gctg gctg gctg gctg gctg -13-
 -14- gctg gctg gctg gctg gctg gctg -14-
 -15- gctg gctg gctg gctg gctg gctg -15-
 -16- gctg gctg gctg gctg gctg gctg -16-
 -17- gctg gctg gctg gctg gctg gctg -17-
 -18- gctg gctg gctg gctg gctg gctg -18-
 -19- gctg gctg gctg gctg gctg gctg -19-
 -20- gctg gctg gctg gctg gctg gctg -20-
 -21- gctg gctg gctg gctg gctg gctg -21-
 -22- gctg gctg gctg gctg gctg gctg -22-
 -23- gctg gctg gctg gctg gctg gctg -23-
 -24- gctg gctg gctg gctg gctg gctg -24-
 -25- gctg gctg gctg gctg gctg gctg -25-
 -26- gctg gctg gctg gctg gctg gctg -26-
 -27- gctg gctg gctg gctg gctg gctg -27-
 -28- gctg gctg gctg gctg gctg gctg -28-
 -29- gctg gctg gctg gctg gctg gctg -29-
 -30- gctg gctg gctg gctg gctg gctg -30-
 -31- gctg gctg gctg gctg gctg gctg -31-
 -32- gctg gctg gctg gctg gctg gctg -32-
 -33- gctg gctg gctg gctg gctg gctg -33-
 -34- gctg gctg gctg gctg gctg gctg -34-
 -35- gctg gctg gctg gctg gctg gctg -35-
 -36- gctg gctg gctg gctg gctg gctg -36-
 -37- gctg gctg gctg gctg gctg gctg -37-
 -38- gctg gctg gctg gctg gctg gctg -38-
 -39- gctg gctg gctg gctg gctg gctg -39-
 -40- gctg gctg gctg gctg gctg gctg -40-
 -41- gctg gctg gctg gctg gctg gctg -41-
 -42- gctg gctg gctg gctg gctg gctg -42-
 -43- gctg gctg gctg gctg gctg gctg -43-
 -44- gctg gctg gctg gctg gctg gctg -44-
 -45- gctg gctg gctg gctg gctg gctg -45-
 -46- gctg gctg gctg gctg gctg gctg -46-
 -47- gctg gctg gctg gctg gctg gctg -47-
 -48- gctg gctg gctg gctg gctg gctg -48-
 -49- gctg gctg gctg gctg gctg gctg -49-
 -50- gctg gctg gctg gctg gctg gctg -50-
 -51- gctg gctg gctg gctg gctg gctg -51-
 -52- gctg gctg gctg gctg gctg gctg -52-
 -53- gctg gctg gctg gctg gctg gctg -53-
 -54- gctg gctg gctg gctg gctg gctg -54-
 -55- gctg gctg gctg gctg gctg gctg -55-
 -56- gctg gctg gctg gctg gctg gctg -56-
 -57- gctg gctg gctg gctg gctg gctg -57-
 -58- gctg gctg gctg gctg gctg gctg -58-
 -59- gctg gctg gctg gctg gctg gctg -59-
 -60- gctg gctg gctg gctg gctg gctg -60-
 -61- gctg gctg gctg gctg gctg gctg -61-
 -62- gctg gctg gctg gctg gctg gctg -62-
 -63- gctg gctg gctg gctg gctg gctg -63-
 -64- gctg gctg gctg gctg gctg gctg -64-
 -65- gctg gctg gctg gctg gctg gctg -65-
 -66- gctg gctg gctg gctg gctg gctg -66-
 -67- gctg gctg gctg gctg gctg gctg -67-
 -68- gctg gctg gctg gctg gctg gctg -68-
 -69- gctg gctg gctg gctg gctg gctg -69-
 -70- gctg gctg gctg gctg gctg gctg -70-
 -71- gctg gctg gctg gctg gctg gctg -71-
 -72- gctg gctg gctg gctg gctg gctg -72-
 -73- gctg gctg gctg gctg gctg gctg -73-
 -74- gctg gctg gctg gctg gctg gctg -74-
 -75- gctg gctg gctg gctg gctg gctg -75-
 -76- gctg gctg gctg gctg gctg gctg -76-
 -77- gctg gctg gctg gctg gctg gctg -77-
 -78- gctg gctg gctg gctg gctg gctg -78-
 -79- gctg gctg gctg gctg gctg gctg -79-
 -80- gctg gctg gctg gctg gctg gctg -80-
 -81- gctg gctg gctg gctg gctg gctg -81-
 -82- gctg gctg gctg gctg gctg gctg -82-
 -83- gctg gctg gctg gctg gctg gctg -83-
 -84- gctg gctg gctg gctg gctg gctg -84-
 -85- gctg gctg gctg gctg gctg gctg -85-
 -86- gctg gctg gctg gctg gctg gctg -86-
 -87- gctg gctg gctg gctg gctg gctg -87-
 -88- gctg gctg gctg gctg gctg gctg -88-
 -89- gctg gctg gctg gctg gctg gctg -89-
 -90- gctg gctg gctg gctg gctg gctg -90-
 -91- gctg gctg gctg gctg gctg gctg -91-
 -92- gctg gctg gctg gctg gctg gctg -92-
 -93- gctg gctg gctg gctg gctg gctg -93-
 -94- gctg gctg gctg gctg gctg gctg -94-
 -95- gctg gctg gctg gctg gctg gctg -95-
 -96- gctg gctg gctg gctg gctg gctg -96-
 -97- gctg gctg gctg gctg gctg gctg -97-
 -98- gctg gctg gctg gctg gctg gctg -98-
 -99- gctg gctg gctg gctg gctg gctg -99-
 -100- gctg gctg gctg gctg gctg gctg -100-

gctccgtggc gggaccctga gctgctggag gggacctgca ccccggtgca 250
 gctggctgcc ctcatctgcc acggcaccgc ctacccacgc gtcaaacaga 300
 tccgcaagct gaggcagctg cacgggttgc tgcaggccgc cgggtccagg 350
 gatggcgggg ctagtagtac cggcagccgc gacctgggtg cagcgtggc 400
 cgactggcct ttgtggtacg cggactggat ggacgggcag ctagtagaga 450
 agggacggca ggatatgca cagctggcgc tgcgtctggc ctgctcttc 500
 ccggcccttt tcagccgtga gaactacggc cgctgcggc tcatcaccag 550
 ttccaagcac cgctgcatgg atagcagcgc cgcttctctg caggggctgt 600
 ggcagcacta ccaccctggc ttgccgcgc cggacgtcgc agatatggag 650
 tttggacctc caacagttaa tgataaacta atgagatttt ttgatcactg 700
 tgagaagttt ttaactgaag tagaaaaaaa tgctacagct ctttatcag 750
 tgggaagcctt caaaactgga ccagaaatgc agaactttt aaaaaagtt 800
 gcagctactt tgcaagtgc agtaaagat ttaaagcag atttaattca 850
 agtagccttt ttcacctgtt catttgacct ggcaattaaa ggtgttaaat 900
 ctcttggtg tgatgttttt gacatagatg atgcaaaggt attagaatat 950
 ttaaagatc tgaaacaata ttggaaaaga ggatatgggt atactattaa 1000
 cagtcgatcc agctgcacct tgtttcagga tatctttcag cacttggaca 1050
 aagcagttga acagaaacaa aggtctcagc caattttctt ccagtcact 1100
 ctccagtttg gtcatgcaga gactctctt ccactgcttt ctctcatggg 1150
 ctacttcaaa gacaaggaac ccctaacagc gtacaattac aaaaaacaaa 1200
 tgcacggaa gttccgaagt ggtctcattg taccttatgc ctggaacctg 1250
 atatttgctg ttaccactg tgaaaatgct aagactcta aagaacaatt 1300
 ccgagtgcag atgtatttaa atgaaaaggt gttacctttg gttactcac 1350
 aagaaactgt ttcattttat gaagatctga agaaccacta caaggacatc 1400
 cttcagagtt gtcaaaccag tgaagaatgt gaattagcaa gggctaacag 1450
 tacatctgat gaactatgag taactgaaga acatttttaa ttcttttagga 1500
 atctgcaatg agtgattaca tgcttgtaat aggtaggcaa ttccttgatt 1550
 acaggaagct tttatattac ttgagtattt ctgtcttttc acagaaaaac 1600
 attgggtttc tctctgggtt tggacatgaa atgtaagaaa agatttttca 1650

ctggagcagc tctcttaagg agaaacaaat ctatttagag aaacagctgg 1700
 ccoctgcaa at gtttacagaa atgaaattct tcctacttat ataagaaatc 1750
 tcacactgag atagaattgt gatttcataa taacacttga aaagtgtctg 1800
 agtaacaaaa tatctcagtt ggaccatcct taacttgatt gaactgtcta 1850
 ggaactttac agattgttct gcagttctct cttcttttcc tcaggttaga 1900
 cagctctagc attttcttaa tcaggaatat tgtggtaagc tgggagtatc 1950
 actctggaag aaagtaacat ctccagatga gaatttgaaa caagaaacag 2000
 agtggtgtaa aaggacacct tcactgaagc aagtcggaaa gtacaatgaa 2050
 aataaatatt tttgggtattt atttatgaaa tatttgaaca ttttttcaat 2100
 aattcctttt tactttctagg aagtctcaaa agaccatctt aaattattat 2150
 atgtttggac aattagcaac aagtcagata gttagaatcg aagtttttca 2200
 aatccattgc ttagctaact ttttcattct gtcacttggc ttcgattttt 2250
 atattttcct attatatgaa atgtatcttt tggttgtttg atttttcttt 2300
 ctttctttgt aaatagttct gagttctgtc aaatgccgtg aaagtatttg 2350
 ctataataaa gaaaattctt gtgactttaa aaaaaaa 2387

<210> 18

<211> 487

<212> PRT

<213> Homo sapiens

<400> 18

Met	Leu	Arg	Ala	Pro	Gly	Cys	Leu	Leu	Arg	Thr	Ser	Val	Ala	Pro
1				5					10					15

Ala	Ala	Ala	Leu	Ala	Ala	Ala	Leu	Leu	Ser	Ser	Leu	Ala	Arg	Cys
			20						25					30

Ser	Leu	Leu	Glu	Pro	Arg	Asp	Pro	Val	Ala	Ser	Ser	Leu	Ser	Pro
			35						40					45

Tyr	Phe	Gly	Thr	Lys	Thr	Arg	Tyr	Glu	Asp	Val	Asn	Pro	Val	Leu
			50						55					60

Leu	Ser	Gly	Pro	Glu	Ala	Pro	Trp	Arg	Asp	Pro	Glu	Leu	Leu	Glu
			65						70					75

Gly	Thr	Cys	Thr	Pro	Val	Gln	Leu	Val	Ala	Leu	Ile	Arg	His	Gly
			80						85					90

Thr	Arg	Tyr	Pro	Thr	Val	Lys	Gln	Ile	Arg	Lys	Leu	Arg	Gln	Leu
			95						100					105

His	Gly	Leu	Leu	Gln	Ala	Arg	Gly	Ser	Arg	Asp	Gly	Gly	Ala	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

110 115 120
 Ser Thr Gly Ser Arg Asp Leu Gly Ala Ala Leu Ala Asp Trp Pro
 125 130 135
 Leu Trp Tyr Ala Asp Trp Met Asp Gly Gln Leu Val Glu Lys Gly
 140 145 150
 Arg Gln Asp Met Arg Gln Leu Ala Leu Arg Leu Ala Ser Leu Phe
 155 160 165
 Pro Ala Leu Phe Ser Arg Glu Asn Tyr Gly Arg Leu Arg Leu Ile
 170 175 180
 Thr Ser Ser Lys His Arg Cys Met Asp Ser Ser Ala Ala Phe Leu
 185 190 195
 Gln Gly Leu Trp Gln His Tyr His Pro Gly Leu Pro Pro Pro Asp
 200 205 210
 Val Ala Asp Met Glu Phe Gly Pro Pro Thr Val Asn Asp Lys Leu
 215 220 225
 Met Arg Phe Phe Asp His Cys Glu Lys Phe Leu Thr Glu Val Glu
 230 235 240
 Lys Asn Ala Thr Ala Leu Tyr His Val Glu Ala Phe Lys Thr Gly
 245 250 255
 Pro Glu Met Gln Asn Ile Leu Lys Lys Val Ala Ala Thr Leu Gln
 260 265 270
 Val Pro Val Asn Asp Leu Asn Ala Asp Leu Ile Gln Val Ala Phe
 275 280 285
 Phe Thr Cys Ser Phe Asp Leu Ala Ile Lys Gly Val Lys Ser Pro
 290 295 300
 Trp Cys Asp Val Phe Asp Ile Asp Asp Ala Lys Val Leu Glu Tyr
 305 310 315
 Leu Asn Asp Leu Lys Gln Tyr Trp Lys Arg Gly Tyr Gly Tyr Thr
 320 325 330
 Ile Asn Ser Arg Ser Ser Cys Thr Leu Phe Gln Asp Ile Phe Gln
 335 340 345
 His Leu Asp Lys Ala Val Glu Gln Lys Gln Arg Ser Gln Pro Ile
 350 355 360
 Ser Ser Pro Val Ile Leu Gln Phe Gly His Ala Glu Thr Leu Leu
 365 370 375
 Pro Leu Leu Ser Leu Met Gly Tyr Phe Lys Asp Lys Glu Pro Leu
 380 385 390
 Thr Ala Tyr Asn Tyr Lys Lys Gln Met His Arg Lys Phe Arg Ser
 395 400 405

Gly	Leu	Ile	Val	Pro	Tyr	Ala	Ser	Asn	Leu	Ile	Phe	Val	Leu	Tyr	410	415	420
His	Cys	Glu	Asn	Ala	Lys	Thr	Pro	Lys	Glu	Gln	Phe	Arg	Val	Gln	425	430	435
Met	Leu	Leu	Asn	Glu	Lys	Val	Leu	Pro	Leu	Ala	Tyr	Ser	Gln	Glu	440	445	450
Thr	Val	Ser	Phe	Tyr	Glu	Asp	Leu	Lys	Asn	His	Tyr	Lys	Asp	Ile	455	460	465
Leu	Gln	Ser	Cys	Gln	Thr	Ser	Glu	Glu	Cys	Glu	Leu	Ala	Arg	Ala	470	475	480
Asn	Ser	Thr	Ser	Asp	Glu	Leu									485		

<210> 19

<211> 3554

<212> DNA

<213> Homo sapiens

<400> 19

```

gggactacaa gccgcgcgcg gctgccgctg gcccctcagc aaccctcgac 50
atggcgctga ggcgccacc gcgactccgg ctctgcgctc ggctgcctga 100
ctttctctctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150
tcaaattccag caatcgaacc ccagtggtag aggaatttga aagtgtggaa 200
ctgtcttgca tcattacgga ttgcgagaca agtgacccca ggatcgagtg 250
gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300
ttcagggaga cttggcggtt cgtgcagaaa tactggggaa gacatccctg 350
aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400
cgttgctcga aatgaccgca aggaaattga tgagattgtg atcgagttaa 450
ctgtgcaagt gaagccagt acccctgtct gtagagtgcc gaaggctgta 500
ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550
ccggcctcac tacagctggt atcgcaatga tgtaccactg cccacggatt 600
ccagagccaa tcccagattt cgcaattctt ctttccactt aaactctgaa 650
acaggcactt tgggtgttcac tgcgtttcac aaggacgact ctgggcagta 700
ctactgcatt gcttccaatg acgcaggctc agccagggtg gaggagcagg 750
agatggaagt ctatgacctg aacattggcg gaattattgg gggggttctg 800
gttgctcttg ctgtactggc cctgatcacg ttgggcatct gctgtgcata 850

```


Met Ala Leu Arg Arg Pro Pro Arg Leu Arg Leu Cys Ala Arg Leu
 1 5 10 15
 Pro Asp Pheⁿ Phe Leu Leu Leu Leu Phe Arg Gly Cys Leu Ile Gly
 20 25 30
 Ala Val Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu
 35 40 45
 Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr
 50 55 60
 Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr
 65 70 75
 Thr Tyr Val Phe Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly
 80 85 90
 Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val
 95 100 105
 Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg
 110 115 120
 Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val
 125 130 135
 Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val
 140 145 150
 Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly
 155 160 165
 His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu
 170 175 180
 Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe
 185 190 195
 His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His
 200 205 210
 Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala
 215 220 225
 Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu
 230 235 240
 Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val
 245 250 255
 Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly
 260 265 270
 Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro
 275 280 285
 Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly

290

295

300

Asp Phe Arg His Lys Ser Ser Phe Val Ile
305 310

<210> 21

<211> 3437

<212> DNA

<213> Homo sapiens

<400> 21

caggaccagg tcttctacg ctggagcagc ggggagacag ccaccatgca 50
catcctcgtg gtccatgcc a tggatgacct gctgacgctg ggcccgcctc 100
gagccgacga cagcgagttc caggcgctgc tggacatctg gtttcggag 150
gagaagccac tgcccaccgc cttcctggtg gacacatcgg aggaggcgct 200
gctgcttct gactggctga agctgcgcat gatccgttct gaggtgctcc 250
gcctgggtgga cgccgccctg caggacctgg agccgcagca gctgctgctg 300
ttcgtgcagt cgtttggcat ccccggtgcc agcatgagca aactcctcca 350
gttctggac caggcagtgg ccacgaccc ccagactctg gagcagaaca 400
tcattggaaa gaattacatg gccacacctg tggagggtcca gcatgagcgc 450
ggcgccctcg gaggccagac ttccactcc ttgctcacag cctccctgcc 500
gccccgccga gacagcacag aggcacccaa accaaagagc agcccagagc 550
agcccatagg ccaggggccg attcgggtgg ggaccagct ccgggtgctg 600
ggccctgagg acgacctggc tggcatgttc ctccagattt tcccgtcag 650
cccggacct cgggtggcaga gctccagtc ccgccccgtg gccctcgccc 700
tgcagcaggc cctgggccag gagctggccc gcgtcgtcca gggcagcccc 750
gaggtgccgg gcatcacggt gcgtgtcctg caggccctcg ccacctgct 800
cagctcccca cagggcgggt cctgggtgat gtccatgcac cgtagccact 850
tctggcctg cccgctgctg cgccagctct gccagtacca gcgtgtgtg 900
ccacaggaca ccggcttctc ctgctcttc ctgaagggtg tctgcagat 950
gctgcagtgg ctggacagcc ctggcggtga gggcgggccc ctgcgggcac 1000
agctcaggat gcttgccagc caggcctcag ccggggcgag gctcagtgat 1050
gtgcgagggg ggctcctgcg cctggccgag gccctggcct tccgtcagga 1100
cctggaggtg gtcagctcca ccgtccgtgc cgtcatcgcc accctgaggt 1150
ctggggagca gtgcagcgtg gagccggacc tgatcagcaa agtcctccag 1200

ccttgccccc ggtcagcgtc tccctgttca cccctctgac cgcggccgag 2700
 atggccccc acatgaaacg gctttcccgg ggccaaacgg tggaggatct 2750
 gctggagggt ctgagtgaca tagacgagat gtcccggcgg agacccgaga 2800
 tccctgagctt cttctcgacc aacctgcagc ggctgatgag ctccggccgag 2850
 gagtgttgcc gcaacctcgc cttcagcctg gccctgcgct ccatgcagaa 2900
 cagcccccagc attgcagccg ctttctctgcc cacgttcatg tactgcctgg 2950
 gcagccagga ctttgagggt gtgcagacgg ccctccggaa cctgcctgag 3000
 tacgtctctc tgtgccaaga gcacgcggct gtgctgctcc accgggcctt 3050
 cctgggtgggc atgtacggcc agatggacc cagcgcgcag atctccgagg 3100
 ccctgaggat cctgcatatg gaggccgtga tgtgagcctg tggcagccga 3150
 cccccctcca agccccggcc cgtcccgtcc ccgggggatcc tcgaggcaaa 3200
 gccaggaag cgtgggcgtt gctggtctgt ccgaggaggt gagggcgcgc 3250
 agccctgagg ccaggcaggc ccaggagcaa tactccgagc cctgggggtgg 3300
 ctccgggcgc gccgctggca tcaggggcgc tccagcaagc cctcattcac 3350
 cttctgggcc acagccctgc cgcggagcgg cggatcccc cgggcattggc 3400
 ctgggctggt tttgaatgaa acgacctgaa ctgtcaa 3437

<210> 22

<211> 1029

<212> PRT

<213> Homo sapiens

<400> 22

Met	His	Ile	Leu	Val	Val	His	Ala	Met	Val	Ile	Leu	Leu	Thr	Leu
1				5					10					15
Gly	Pro	Pro	Arg	Ala	Asp	Asp	Ser	Glu	Phe	Gln	Ala	Leu	Leu	Asp
				20					25					30
Ile	Trp	Phe	Pro	Glu	Glu	Lys	Pro	Leu	Pro	Thr	Ala	Phe	Leu	Val
				35					40					45
Asp	Thr	Ser	Glu	Glu	Ala	Leu	Leu	Leu	Pro	Asp	Trp	Leu	Lys	Leu
				50					55					60
Arg	Met	Ile	Arg	Ser	Glu	Val	Leu	Arg	Leu	Val	Asp	Ala	Ala	Leu
				65					70					75
Gln	Asp	Leu	Glu	Pro	Gln	Gln	Leu	Leu	Leu	Phe	Val	Gln	Ser	Phe
				80					85					90
Gly	Ile	Pro	Val	Ser	Ser	Met	Ser	Lys	Leu	Leu	Gln	Phe	Leu	Asp
				95					100					105

	395	400	405
Thr Ala Asp Ala	Ala Ser Pro Phe Pro	Ala Cys Lys Pro Val	Val
	410	415	420
Val Val Ser Ser	Leu Leu Leu Gln Glu	Glu Glu Pro Leu Ala	Gly
	425	430	435
Gly Lys Pro Gly	Ala Asp Gly Gly Ser	Leu Glu Ala Val Arg	Leu
	440	445	450
Gly Pro Ser Ser	Gly Leu Leu Val Asp	Trp Leu Glu Met Leu	Asp
	455	460	465
Pro Glu Val Val	Ser Ser Cys Pro Asp	Leu Gln Leu Arg Leu	Leu
	470	475	480
Phe Ser Arg Arg	Lys Gly Lys Gly Gln	Ala Gln Val Pro Ser	Phe
	485	490	495
Arg Pro Tyr Leu	Leu Thr Leu Phe Thr	His Gln Ser Ser Trp	Pro
	500	505	510
Thr Leu His Gln	Cys Ile Arg Val Leu	Leu Gly Lys Ser Arg	Glu
	515	520	525
Gln Arg Phe Asp	Pro Ser Ala Ser Leu	Asp Phe Leu Trp Ala	Cys
	530	535	540
Ile His Val Pro	Arg Ile Trp Gln Gly	Arg Asp Gln Arg Thr	Pro
	545	550	555
Gln Lys Arg Arg	Glu Glu Leu Val Leu	Arg Val Gln Gly Pro	Glu
	560	565	570
Leu Ile Ser Leu	Val Glu Leu Ile Leu	Ala Glu Ala Glu Thr	Arg
	575	580	585
Ser Gln Asp Gly	Asp Thr Ala Ala Cys	Ser Leu Ile Gln Ala	Arg
	590	595	600
Leu Pro Leu Leu	Leu Ser Cys Cys Cys	Gly Asp Asp Glu Ser	Val
	605	610	615
Arg Lys Val Thr	Glu His Leu Ser Gly	Cys Ile Gln Gln Trp	Gly
	620	625	630
Asp Ser Val Leu	Gly Arg Arg Cys Arg	Asp Leu Leu Leu Gln	Leu
	635	640	645
Tyr Leu Gln Arg	Pro Glu Leu Arg Val	Pro Val Pro Glu Val	Leu
	650	655	660
Leu His Ser Glu	Gly Ala Ala Ser Ser	Ser Val Cys Lys Leu	Asp
	665	670	675
Gly Leu Ile His	Arg Phe Ile Thr Leu	Leu Ala Asp Thr Ser	Asp
	680	685	690

Ser Arg Ala Leu Glu Asn Arg Gly Ala Asp Ala Ser Met Ala Cys	695	700	705
Arg Lys Leu Ala Val Ala His Pro Leu Leu Leu Leu Arg His Leu	710	715	720
Pro Met Ile Ala Ala Leu Leu His Gly Arg Thr His Leu Asn Phe	725	730	735
Gln Glu Phe Arg Gln Gln Asn His Leu Ser Cys Phe Leu His Val	740	745	750
Leu Gly Leu Leu Glu Leu Leu Gln Pro His Val Phe Arg Ser Glu	755	760	765
His Gln Gly Ala Leu Trp Asp Cys Leu Leu Ser Phe Ile Arg Leu	770	775	780
Leu Leu Asn Tyr Arg Lys Ser Ser Arg His Leu Ala Ala Phe Ile	785	790	795
Asn Lys Phe Val Gln Phe Ile His Lys Tyr Ile Thr Tyr Asn Ala	800	805	810
Pro Ala Ala Ile Ser Phe Leu Gln Lys His Ala Asp Pro Leu His	815	820	825
Asp Leu Ser Phe Asp Asn Ser Asp Leu Val Met Leu Lys Ser Leu	830	835	840
Leu Ala Gly Leu Ser Leu Pro Ser Arg Asp Asp Arg Thr Asp Arg	845	850	855
Gly Leu Asp Glu Glu Gly Glu Glu Glu Ser Ser Ala Gly Ser Leu	860	865	870
Pro Leu Val Ser Val Ser Leu Phe Thr Pro Leu Thr Ala Ala Glu	875	880	885
Met Ala Pro Tyr Met Lys Arg Leu Ser Arg Gly Gln Thr Val Glu	890	895	900
Asp Leu Leu Glu Val Leu Ser Asp Ile Asp Glu Met Ser Arg Arg	905	910	915
Arg Pro Glu Ile Leu Ser Phe Phe Ser Thr Asn Leu Gln Arg Leu	920	925	930
Met Ser Ser Ala Glu Glu Cys Cys Arg Asn Leu Ala Phe Ser Leu	935	940	945
Ala Leu Arg Ser Met Gln Asn Ser Pro Ser Ile Ala Ala Ala Phe	950	955	960
Leu Pro Thr Phe Met Tyr Cys Leu Gly Ser Gln Asp Phe Glu Val	965	970	975
Val Gln Thr Ala Leu Arg Asn Leu Pro Glu Tyr Ala Leu Leu Cys			

980	985	990
Gln Glu His Ala Ala Val Leu Leu His Arg Ala Phe Leu Val Gly		
995	1000	1005
Met Tyr Gly Gln Met Asp Pro Ser Ala Gln Ile Ser Glu Ala Leu		
1010	1015	1020
Arg Ile Leu His Met Glu Ala Val Met		
1025		

<210> 23
 <211> 2186
 <212> DNA
 <213> Homo sapiens

<400> 23
 ccggggccatg cagcctcggc cccgcgggcg cccgcccgcg acccgaggag 50
 atgaggctcc gcaatggcac ctctctgacg ctgctgctct tctgcctgtg 100
 cgccttctctc tcgctgtcct ggtaacgcggc actcagcggc cagaaaggcg 150
 acgttgtgga cgtttaccag cgggagttcc tggcgctgcg cgatcggttg 200
 cacgcagctg agcaggagag cctcaagcgc tccaaggagc tcaacctggg 250
 gctggacgag atcaagaggg ccgtgtcaga aaggcaggcg ctgcgagacg 300
 gagacggcaa tcgcacctgg ggccgcctaa cagaggacct ccgattgaag 350
 ccgtggaacg gctcacaccg gcacgtgctg cacctgcca ccgtcttcca 400
 tcacctgcca cacctgtggt ccaaggagag cagtctgcag cccgcgggtgc 450
 gcgtgggcca gggccgcacc ggagtgtcgg tggatgatgg catcccgagc 500
 gtgcggcgcg aggtgcactc gtacctgact gacactctgc actcgctcat 550
 ctccgagctg agcccgcagg agaaggagga ctcggtcatc gtggtgctga 600
 tcgccgagac tgactcacag tacacttcgg cagtgcaga gaacatcaag 650
 gccttgttcc ccacggagat ccattctggg ctcttgagg tcatctcacc 700
 ctccccccac ttctaccctg acttctcccg cctccgagag tcctttgggg 750
 accccaaagg gagagtcagg tggaggacca aacagaacct cgattactgc 800
 ttctctcatg tgtacgcgca gtccaaaggc atctactacg tgcagctgga 850
 ggatgacatc gtggccaagc ccaactacct gagcaccatg aagaactttg 900
 cactgcagca gccttcagag gactggatga tcctggagtt ctcccagctg 950
 ggcttcattg gtaagatgtt caagtcgctg gacctgagcc tgattgtaga 1000
 gttcattctc atgttctacc gggacaagcc catcgactgg ctcttgagcc 1050

atattctgtg ggtgaaagtc tgcaaccccg agaaggatgc gaagcaactgt 1100
 gaccggcaga aagccaacct gcggatccgc ttcaaaccgt ccctcttcca 1150
 gcacgtgggc actcactcct cgctggctgg caagatccag aaactgaagg 1200
 acaaagactt tggaaagcag gcgctgcgga aggagcatgt gaacccgcca 1250
 gcagagggtga gcacgagcct gaagacatac cagcacttca ccctggagaa 1300
 agcctacctg cgcgaggact tcttctgggc cttcaccctt gccgcggggg 1350
 acttcatccg cttccgcttc ttccaacctc taagactgga gcggttcttc 1400
 ttccgcagtg ggaacatcga gcaccgggag gacaagctct tcaacacgtc 1450
 tgtggagggtg ctgcccttcg acaaacctca gtcagacaag gaggccctgc 1500
 aggagggccg caccgccacc ctccggtacc ctcgagccc cgacggctac 1550
 ctccagatcg gctccttcta caagggagtg gcagaggag aggtggacce 1600
 agccttcggc cctctggaag cactgcgctt ctgatccag acggactccc 1650
 ctgtgtgggt gattctgagc gagatcttcc tgaaaaaggc cgactaagct 1700
 gcgggcttct gaggggtacc tgtggccagc cctgaagccc acatttctgg 1750
 ggggtgtcgtc actgccgtcc ccggagggcc agatacggcc ccgccc aaag 1800
 ggttctgctt ggcgtcgggc ttgggcccgc ctgggggtccg ccgctggccc 1850
 ggaggcccta ggagctgggt ctgccccgc ccgcccgggc gcggaggagg 1900
 caggcggccc ccacactgtg cctgagggcc ggaaccgttc gcaccggccc 1950
 tgccccagtc aggcggtttt agaagagctt ttacttgggc gcccgccgtc 2000
 tctggcgaga aacttggaat gcatatacta ctttatgtgc tgtgtttttt 2050
 attcttgat acatttgatt ttttcacgta agtccacata tactttctata 2100
 agagcgtgac ttgtaataaa gggttaatga agaaaaaaaa aaaaaaaaaa 2150
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2186

<210> 24

<211> 548

<212> PRT

<213> Homo sapiens

<400> 24

Met	Arg	Leu	Arg	Asn	Gly	Thr	Phe	Leu	Thr	Leu	Leu	Leu	Phe	Cys
1				5					10					15
Leu	Cys	Ala	Phe	Leu	Ser	Leu	Ser	Trp	Tyr	Ala	Ala	Leu	Ser	Gly
				20					25					30

Gln	Lys	Gly	Asp	Val	Val	Asp	Val	Tyr	Gln	Arg	Glu	Phe	Leu	Ala	35	40	45
Leu	Arg	Asp	Arg	Leu	His	Ala	Ala	Glu	Gln	Glu	Ser	Leu	Lys	Arg	50	55	60
Ser	Lys	Glu	Leu	Asn	Leu	Val	Leu	Asp	Glu	Ile	Lys	Arg	Ala	Val	65	70	75
Ser	Glu	Arg	Gln	Ala	Leu	Arg	Asp	Gly	Asp	Gly	Asn	Arg	Thr	Trp	80	85	90
Gly	Arg	Leu	Thr	Glu	Asp	Pro	Arg	Leu	Lys	Pro	Trp	Asn	Gly	Ser	95	100	105
His	Arg	His	Val	Leu	His	Leu	Pro	Thr	Val	Phe	His	His	Leu	Pro	110	115	120
His	Leu	Leu	Ala	Lys	Glu	Ser	Ser	Leu	Gln	Pro	Ala	Val	Arg	Val	125	130	135
Gly	Gln	Gly	Arg	Thr	Gly	Val	Ser	Val	Val	Met	Gly	Ile	Pro	Ser	140	145	150
Val	Arg	Arg	Glu	Val	His	Ser	Tyr	Leu	Thr	Asp	Thr	Leu	His	Ser	155	160	165
Leu	Ile	Ser	Glu	Leu	Ser	Pro	Gln	Glu	Lys	Glu	Asp	Ser	Val	Ile	170	175	180
Val	Val	Leu	Ile	Ala	Glu	Thr	Asp	Ser	Gln	Tyr	Thr	Ser	Ala	Val	185	190	195
Thr	Glu	Asn	Ile	Lys	Ala	Leu	Phe	Pro	Thr	Glu	Ile	His	Ser	Gly	200	205	210
Leu	Leu	Glu	Val	Ile	Ser	Pro	Ser	Pro	His	Phe	Tyr	Pro	Asp	Phe	215	220	225
Ser	Arg	Leu	Arg	Glu	Ser	Phe	Gly	Asp	Pro	Lys	Glu	Arg	Val	Arg	230	235	240
Trp	Arg	Thr	Lys	Gln	Asn	Leu	Asp	Tyr	Cys	Phe	Leu	Met	Met	Tyr	245	250	255
Ala	Gln	Ser	Lys	Gly	Ile	Tyr	Tyr	Val	Gln	Leu	Glu	Asp	Asp	Ile	260	265	270
Val	Ala	Lys	Pro	Asn	Tyr	Leu	Ser	Thr	Met	Lys	Asn	Phe	Ala	Leu	275	280	285
Gln	Gln	Pro	Ser	Glu	Asp	Trp	Met	Ile	Leu	Glu	Phe	Ser	Gln	Leu	290	295	300
Gly	Phe	Ile	Gly	Lys	Met	Phe	Lys	Ser	Leu	Asp	Leu	Ser	Leu	Ile	305	310	315
Val	Glu	Phe	Ile	Leu	Met	Phe	Tyr	Arg	Asp	Lys	Pro	Ile	Asp	Trp			

320	325	330
Leu Leu Asp His Ile Leu Trp Val Lys Val Cys Asn Pro Glu Lys		
335	340	345
Asp Ala Lys His Cys Asp Arg Gln Lys Ala Asn Leu Arg Ile Arg		
350	355	360
Phe Lys Pro Ser Leu Phe Gln His Val Gly Thr His Ser Ser Leu		
365	370	375
Ala Gly Lys Ile Gln Lys Leu Lys Asp Lys Asp Phe Gly Lys Gln		
380	385	390
Ala Leu Arg Lys Glu His Val Asn Pro Pro Ala Glu Val Ser Thr		
395	400	405
Ser Leu Lys Thr Tyr Gln His Phe Thr Leu Glu Lys Ala Tyr Leu		
410	415	420
Arg Glu Asp Phe Phe Trp Ala Phe Thr Pro Ala Ala Gly Asp Phe		
425	430	435
Ile Arg Phe Arg Phe Phe Gln Pro Leu Arg Leu Glu Arg Phe Phe		
440	445	450
Phe Arg Ser Gly Asn Ile Glu His Pro Glu Asp Lys Leu Phe Asn		
455	460	465
Thr Ser Val Glu Val Leu Pro Phe Asp Asn Pro Gln Ser Asp Lys		
470	475	480
Glu Ala Leu Gln Glu Gly Arg Thr Ala Thr Leu Arg Tyr Pro Arg		
485	490	495
Ser Pro Asp Gly Tyr Leu Gln Ile Gly Ser Phe Tyr Lys Gly Val		
500	505	510
Ala Glu Gly Glu Val Asp Pro Ala Phe Gly Pro Leu Glu Ala Leu		
515	520	525
Arg Leu Ser Ile Gln Thr Asp Ser Pro Val Trp Val Ile Leu Ser		
530	535	540
Glu Ile Phe Leu Lys Lys Ala Asp		
545		

<210> 25

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 25

tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 26
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 26
 caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

 <210> 27
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 27
 actcgggatt cctgctgtt 19

 <210> 28
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 28
 aggcctttac ccaaggccac aac 23

 <210> 29
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 29
 ggcctgtcct gtgtttctca 19

 <210> 30
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 30
 tcccaccact tacttccatg aa 22

 <210> 31
 <211> 25
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 31

ctgtggtacc caattgcegc cttgt 25

<210> 32

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 32

attgtcctga gattcgagca aga 23

<210> 33

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 33

gtccagcaag ccctcatt 18

<210> 34

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 34

cttctgggcc acagccctgc 20

<210> 35

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 35

cagttcaggt cgtttcattc a 21

<210> 36

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 36

ccagtcaggc cgttttaga 19

<210> 37

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 37

cgggcgcca agtaaaagct c 21

<210> 38

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 38

cataaagtag tatatgcatt ccagtggt 28